In the Specification:

Applicants respectfully request entry of the attached amended sequence listing, dated March 2, 2006, in the instant specification, to replace the current sequence listing on file.

Please amend the paragraph starting on Page7, line 23 of the specification as follows:

FIG. 11. Primary structural comparison of STEAP family proteins. FIG. 11A. Amino acid sequence alignment of STEAP-1 ~~(8P1D4 CLONE 10; SEQ ID NO: 1)~~ (8P1D4 CLONE 10; SEQ ID NO:2) and STEAP-2 ~~(98P4B6; SEQ ID NO: 7)~~ (98P4B6; SEQ ID NO:8) sequences. The alignment was performed using the SIM alignment program of the Baylor College of Medicine Search Launcher Web site. Results show a 61.4% identity in a 171 amino acid overlap; Score: 576.0; Gap frequency: 0.0%. FIG. 11B. Amino acid sequence alignment of STEAP-1 with partial ORF sequences of STEAP-2 and two other putative family member proteins (SEQ ID NO:33 and SEQ ID NO:34) using the PIMA program ~~(PIMA 1.4 program at Internet address http://dot.imgen.bcm.tmc.edu:9331\multi-align\multi-align.html)~~; transmembrane domains identified by the SOSUI program ~~(available at Internet address <http://www.tuat.ac.jp\~mitaku\adv_sosui\submit.html>)~~ are in bold.

Please amend the paragraph starting on Page 18, line 8 of the specification as follows:

A specific embodiment of a STEAP protein comprises a polypeptide having the amino acid sequence of human STEAP-1 as shown in FIG. 1A (SEQ ID NO. 2). Another embodiment of a STEAP protein comprises a polypeptide containing the partial STEAP-2 amino acid sequence as shown in FIG. 9 (SEQ ID NO. 8). Another embodiment comprises a polypeptide containing the partial STEAP-3 amino acid sequence of (SEQ ID NO:33) shown in FIG. 11B. Yet another embodiment comprises a polypeptide containing the partial STEAP-4 amino acid sequence of (SEQ ID NO:34) shown in FIG. 11B.

Please amend the paragraph starting on Page 19, line 15 of the specification as follows:

The invention also provides STEAP polypeptides comprising biologically active fragments of the STEAP amino acid sequence, such as a polypeptide corresponding to part of the amino acid sequences for STEAP-1 as shown in FIG. 1A (SEQ ID NO. 2), STEAP-2 as shown in FIG. 9 (SEQ ID NO: 8), or STEAP-3 (SEQ ID NO:33), or STEAP-4 (SEQ ID NO:34), as shown

in FIG. 11B. Such polypeptides of the invention exhibit properties of a STEAP protein, such as the ability to elicit the generation of antibodies which specifically bind an epitope associated with a STEAP protein. Polypeptides comprising amino acid sequences which are unique to a particular STEAP protein (relative to other STEAP proteins) may be used to generate antibodies which will specifically react with that particular STEAP protein. For example, referring to the amino acid alignment of the STEAP-1 and STEAP-2 structures shown in FIG. 11A, the skilled artisan will readily appreciate that each molecule contains stretches of sequence unique to its structure. These unique stretches can be used to generate STEAP-1 or STEAP-2 specific antibodies.

Please amend the paragraph starting on Page 37, line 25 of the specification as follows:

Normalization of the first strand cDNAs from multiple tissues was performed by using the primers 5'atatcgccgcgctcgtcgtcgacaa3' (SEQ ID NO: 30) and 5'agccacacgcagctcattgtagaagg3' (SEQ ID NO: 31) to amplify β-actin. First strand cDNA (5 μl) was amplified in a total volume of 50 μl containing 0.4 μM primers, 0.2 μM each dNTPs, 1XPCR buffer (Clontech, 10 mM Tris-HCL, 1.5 mM MgCl.sub.2, 50 mM KCl, pH8.3) and 1X Klentaq DNA polymerase (Clontech). Five μl of the PCR reaction was removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycler under the following conditions: initial denaturation was at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 bp β-actin bands from multiple tissues were compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal β-actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization were required to achieve equal band intensities in all tissues after 22 cycles of PCR.

Please amend the paragraph starting on Page 41, line 16 of the specification as follows:

A 15 mer peptide corresponding to amino acid residues 14 through 28 of the STEAP-1 amino acid sequence as shown in FIG. 1A (WKMKPRRNLEEDDYL) ~~(SEQ ID NO: 2)~~ (SEQ ID NO: 37) was synthesized and used to immunize sheep for the generation of sheep polyclonal

antibodies towards the amino-terminus of the protein (anti-STEAP-1) as follows. The peptide was conjugated to KLH (keyhole limpet hemocyanin). The sheep was initially immunized with 400 .mu.g of peptide in complete Freund's adjuvant. The animal was subsequently boosted every two weeks with 200 .mu.g of peptide in incomplete Freund's adjuvant. Anti-STEAP antibody was affinity-purified from sheep serum using STEAP peptide coupled to Affi-Gel 10 (Bio-Rad). Purified antibody is stored in phosphate-buffered saline with 0.1% sodium azide.

Please amend the paragraph starting on Page 42, line 12 of the specification as follows:

To determine the extent of STEAP-1 protein expression in clinical materials, tissue sections were prepared from a variety of prostate cancer biopsies and surgical samples for immunohistochemical analysis. Tissues were fixed in 10% formalin, embedded in paraffin, and sectioned according to standard protocol. Formalin-fixed, paraffin-embedded sections of LNCaP cells were used as a positive control. Sections were stained with an anti-STEAP-1 polyclonal antibody directed against a STEAP-1 N-terminal epitope (as described immediately above). LNCaP sections were stained in the presence of an excess amount of the STEAP-1 N-terminal peptide immunogen used to generate the polyclonal antibody (peptide 1) or a non-specific peptide derived from a distinct region of the STEAP-1 protein (peptide 2; YQQVQQNKEDAWIEH; (SEQ ID NO: 32)).

Please amend the paragraph starting on Page 48, line 1 of the specification as follows:

The resulting STEAP-1 mapping vector for the 93 radiation hybrid panel DNAs (21000002011010100010000001011101012210001110011101101010001000100010100102100000111100101000), and the mapping program available at the internet address ~~<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>,~~ for the Whitehead Institute for Biomedical Research, localized the STEAP-1 gene to chromosome 7p22.3, telomeric to D7S531.

Please amend the paragraph starting on Page 48, line 12 of the specification as follows:

The resulting vector (00000100100000000000000000000010010000000001000100000000001000010101010010011), and the mapping program available at the internet address

~~<http://www-shgc.stanford.edu/RH/rhserverformnew.html>,~~ for the Stanford Human Genome Center, maps the 98P4B6 (STEAP-2) gene to chromosome 7q21.

Please amend the paragraph starting on Page 48, line 21 of the specification as follows:

The resulting vector (00000000100000000000000000010001000002000000010001000000010001000101000001 0), and the mapping program available at the internet address ~~<http://www-shgc.stanford.edu/RH/rhserverformnew.html>,~~ for the Stanford Human Genome Center, maps AI139607 to chromosome 7q21.

Please amend the paragraph starting on Page 48, line 26 of the specification as follows:

The following PCR primers were used for R80991:

R80991.3 5' ACAAGAGCCACCTCTGGGTGAA 3' ~~(SEQ ID NO:15)~~ (SEQ ID NO: 35)

R80991.4 5' AGTTGAGCGAGTTTGCAATGGAC 3' ~~(SEQ ID NO:16)~~ (SEQ ID NO: 36)

Please amend the paragraph starting on Page 48, line 30 of the specification as follows:

The resulting vector (00000000000200001020000000010000000000000000000010000 0000010000111000000010010000001), and the mapping program available at the internet address ~~<http://www-shgc.stanford.edu/RH/rhserverformnew.html>,~~ for the Stanford Human Genome Center, maps R80991 to chromosome 2q14-q21, near D2S2591.

Please add the following new paragraph immediately after the paragraph at Page 39, lines 9-25:

This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations there under (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit and for at least five (5) years after the most recent request for the furnishing of a sample of the deposit received by the depository. The deposits

will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures that all restrictions imposed by the depositor on the availability to the public of the deposited material will be irrevocably removed upon the granting of the pertinent U.S. patent, assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 U.S.C. §122 and the Commissioner's rules pursuant thereto (including 37 C.F.R. §1.14 with particular reference to 886 OG 638).

Please delete the paragraph that begins at Page 49, line 36, and ends at Page 50, line 3.

Please delete the paragraphs at Page 50, lines 19-48.

Please add the following paragraphs beginning at page 51, line 1:

SEQUENCE LISTING

<110> Afar, Daniel E.
Hubert, Rene S.
Leong, Kahan
Raitano, Arthur B.
Saffran, Douglas C.
Mitchell, Stephen C.

<120> NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS EXPRESSED IN HUMAN CANCERS AND USES THEREOF

<130> 1703-011.US1

<140> US 09/323,873
<141> 1999-06-01

<150> US 60/087,520
<151> 1998-06-01

<150> US 60/091,183

<151> 1998-06-30

<160> 29

<170> PatentIn Ver 2.0

<210> 1
<211> 1195
<212> DNA

Please amend the Abstract as follows:

Described is a novel family of cell surface serpentine transmembrane antigens. Two of the proteins in this family are exclusively or predominantly expressed in the prostate, as well as in prostate cancer, and thus members of this family have been termed ~~"STRAP" (Serpentine Transmembrane Antigens of the Prostate).~~ "STEAP" (Six Transmembrane Epithelial Antigens of the Prostate). Four particular human ~~STRAPs~~ STEAPs are described and characterized herein. The human ~~STRAPs~~ STEAPs exhibit a high degree of structural conservation among them but show no significant structural homology to any known human proteins. The prototype member of the ~~STRAP~~ STEAP family, ~~STRAP-1~~ STEAP-1, appears to be a type IIIa membrane protein expressed predominantly in prostate cells in normal human tissues. Structurally, ~~STRAP-1~~ STEAP-1 is a 339 amino acid protein characterized by a molecular topology of six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. ~~STRAP-1~~ STEAP-1 protein expression is maintained at high levels across various stages of prostate cancer. Moreover, ~~STRAP-1~~ STEAP-1 is highly over-expressed in certain other human cancers.